

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
- (ii) TITLE OF INVENTION: Bacterial Superantigen
Vaccines
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Charles H. Harris
 - (B) STREET: US Army MPMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Atty)
 - (C) CITY: FORT DETRICK
 - (D) STATE: MARYLAND
 - (E) COUNTRY: USA
 - (F) ZIP: 21702-5012
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh 7.5
 - (D) SOFTWARE: Microsoft Word 6.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/882,431
 - (B) FILING DATE: June 25, 1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Charles H. Harris
 - (B) REGISTRATION NUMBER: 34,616
 - (C) REFERENCE/DOCKET NUMBER:
- (ix) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: (301) 619-2065
 - (B) TELEFAX: (301) 619-7714

(2) INFORMATION FOR SEQUENCE ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 830
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAAAAAAAA CAGCATTTAC ATTACTTTTA TTCATTGCCC	40
TAACGTTGAC AACAGTCCA CTTGTAAATG GTAGCGAGAA	80
AAGCGAAGAA ATAAATGAAA AAGATTTGCG AAAAAAGTCT	120
GAATTGCAGG GAACAGCTTT AGGCAATCTT AAACAAATCT	160
ATTATTACAA TGAAAAAGCT AAAACTGAAA ATAAAGAGAG	200
TCACGATCAA TTTCGACAGC ATACTATATT GTTTAAAGGC	240
TTTTTTTACAG ATCATTTCGTG GTATAACGAT TTATTAGTAC	280
GTTTTGATTC AAAGGATATT GTTGATAAAT ATAAAGGGAA	320
AAAAGTAGAC TTGTATGGTG CTTATGCTGG TTATCAATGT	360
GCGGGTGGTA CACCAAACAA AACAGCTTGT ATGTATGGTG	400
GTGTAACGTT ACATGATAAT AATCGATTGA CCGAAGAGAA	440
AAAAGTGCCG ATCAATTTAT GGCTAGACGG TAAACAAAAT	480
ACAGTACCTT TGGAAACGGT TAAAACGAAT AAGAAAAATG	520
TAAGTGTTC GGAGTTGGAT CTTCAAGCAA GACGTTATTT	560
ACAGGAAAAA TATAATTTAT ATAAGTCTGA TGTTTTGGAT	600
GGGAAGGTT AGAGGGGATT AATCGTGTTT CATACTTCTA	640
CAGAACCTTC GGTAAATTAC GATTTATTTG GTGCTCAAGG	680
ACAGTATTCA AATACACTAT TAAGAATATA TAGAGATAAT	720
AAAACGATTA ACTCTGAAAA CATGCATATT GATATATATT	760
TATATACAAG TTAAACATGG TAGTTTGGAC CAACGTAATG	800
TTCAGATTAT TATGAACCGA GAATAATCTA	830

(3) INFORMATION FOR SEQUENCE ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257

(B) TYPE: Amino Acid
 (C) STRANDEDNESS: Unknown
 (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Lys	Thr	Ala	Phe	Thr	Leu	Leu	Leu	1	5	10
Phe	Ile	Ala	Leu	Thr	Leu	Thr	Thr	Ser	Pro	15	20	
Leu	Val	Asn	Gly	Ser	Glu	Lys	Ser	Glu	Glu	25	30	
Ile	Asn	Glu	Lys	Asp	Leu	Arg	Lys	Lys	Ser	35	40	
Glu	Leu	Gln	Gly	Thr	Ala	Leu	Gly	Asn	Leu	45	50	
Lys	Gln	Ile	Tyr	Tyr	Tyr	Asn	Glu	Lys	Ala	55	60	
Lys	Thr	Glu	Asn	Lys	Glu	Ser	His	Asp	Gln	65	70	
Phe	Arg	Gln	His	Thr	Ile	Leu	Phe	Lys	Gly	75	80	
Phe	Phe	Thr	Asp	His	Ser	Trp	Tyr	Asn	Asp	85	90	
Leu	Leu	Val	Arg	Phe	Asp	Ser	Lys	Asp	Ile	95	100	
Val	Asp	Lys	Tyr	Lys	Gly	Lys	Lys	Val	Asp	105	110	
Leu	Tyr	Gly	Ala	Tyr	Ala	Gly	Tyr	Gln	Cys	115	120	
Ala	Gly	Gly	Thr	Pro	Asn	Lys	Thr	Ala	Cys	125	130	
Met	Tyr	Gly	Gly	Val	Thr	Leu	His	Asp	Asn	135	140	
Asn	Arg	Leu	Thr	Glu	Glu	Lys	Lys	Val	Pro	145	150	
Ile	Asn	Leu	Trp	Leu	Asp	Gly	Lys	Gln	Asn	155	160	

Thr	Val	Pro	Leu	Glu	Thr	Val	Lys	Thr	Asn	165	170
Lys	Lys	Asn	Val	Thr	Val	Gln	Glu	Leu	Asp	175	180
Leu	Gln	Ala	Arg	Arg	Tyr	Leu	Gln	Glu	Lys	185	190
Tyr	Asn	Leu	Tyr	Asn	Ser	Asp	Val	Phe	Asp	195	200
Gly	Lys	Val	Gln	Arg	Gly	Leu	Ile	Val	Phe	205	210
His	Thr	Ser	Thr	Glu	Pro	Ser	Val	Asn	Tyr	215	220
Asp	Leu	Phe	Gly	Ala	Gln	Gly	Gln	Tyr	Ser	225	230
Asn	Thr	Leu	leu	Arg	Ile	Tyr	Arg	Asp	Asn	235	240
Lys	Thr	Ile	Asn	Ser	Glu	Asn	Met	His	Ile	245	250
Asp	Ile	Tyr	Leu	Tyr	Thr	Ser				255	

(4) INFORMATION FOR SEQUENCE ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAGAAAAG	CGAAGAAATA	AATGAAAAAG	ATTTGCGAAA	40
AAAGTCTGAA	TTGCAGGGAA	CAGCTTTAGG	CAATCTTAAA	80
CAAATCTATT	ATTACAATGA	AAAAGCTAAA	ACTGAAAATA	120
AAGAGAGTCA	CGATCAATTT	CGACAGCATA	CTATATTGTT	160
TAAAGGCTTT	TTTACAGATC	ATTCGTGGTA	TAACGATTTA	200

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TTAGTACGTT TTGATTCAAA GGATATTGTT GATAAATATA 240
AAGGGAAAAA AGTAGACTTG TATGGTGCTT ATGCTGGTTA 280
TCAATGTGCG GGTGGTACAC CAAACAAAAC AGCTTGATG 320
TATGGTGGTG TAACGTTACA TGATAATAAT CGATTGACCG 360
AAGAGAAAAA AGTGCCGATC AATTTATGGC TAGACGGTAA 400
ACAAAATACA GTACCTTTGG AAACGGTTAA AACGAATAAG 440
AAAAATGTAA CTGTTTCAGGA GTTGGATCTT CAAGCAAGAC 480
GTTATTTTACA GGAAAAATAT AATTTATATA ACTCTGATGT 520
TTTTGATGGG AAGGTTTCAGA GGGGATTAAT CGTGTTCAT 560
ACTTCTACAG AACCTTCGGT TAATTACGAT TTATTTGGTG 600
CTCAAGGACA GTATTCAAAT ACACTATTAA GAATATATAG 640
AGATAATAAA ACGATTAACT CTGAAAACAT GCATATTGAT 680
ATATATTTAT ATACAAGTTA AACATGGTAG TTTTGACCAA 720
CGTAATGTTC AGATTATTAT GAACCGAGAA TAATCTA 757

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(5) INFORMATION FOR SEQUENCE ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:233
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Glu Lys Ser Glu Glu Ile Asn Glu Lys
      5                      10
Asp Leu Arg Lys Lys Ser Glu Leu Gln Gly
      15                     20
Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr
      25                     30
Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn
      35                     40
Lys Glu Ser His Asp Gln Phe Arg Gln His
      45                     50

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Thr	Ile	Leu	Phe	Lys	Gly	Phe	Phe	Thr	Asp		
				55					60		
His	Ser	Trp	Tyr	Asn	Asp	Leu	Leu	Val	Arg		
				65					70		
Phe	Asp	Ser	Lys	Asp	Ile	Val	Asp	Lys	Tyr		
				75					80		
Lys	Gly	Lys	Lys	Val	Asp	Leu	Tyr	Gly	Ala		
				85					90		
Tyr	Ala	Gly	Tyr	Gln	Cys	Ala	Gly	Gly	Thr		
				95					100		
Pro	Asn	Lys	Thr	Ala	Cys	Met	Tyr	Gly	Gly		
				105					110		
Val	Thr	Leu	His	Asp	Asn	Asn	Arg	Leu	Thr		
				115					120		
Glu	Glu	Lys	Lys	Val	Pro	Ile	Asn	Leu	Trp		
				125					130		
Leu	Asp	Gly	Lys	Gln	Asn	Thr	Val	Pro	Leu		
				135					140		
Glu	Thr	Val	Lys	Thr	Asn	Lys	Lys	Asn	Val		
				145					150		
Thr	Val	Gln	Glu	Leu	Asp	Leu	Gln	Ala	Arg		
				155					160		
Arg	Tyr	Leu	Gln	Glu	Lys	Tyr	Asn	Leu	Tyr		
				165					170		
Asn	Ser	Asp	Val	Phe	Asp	Gly	Lys	Val	Gln		
				175					180		
Arg	Gly	Leu	Ile	Val	Phe	His	Thr	Ser	Thr		
				185					190		
Glu	Pro	Ser	Val	Asn	Tyr	Asp	Leu	Phe	Gly		
				195					200		
Ala	Gln	Gly	Gln	Tyr	Ser	Asn	Thr	Leu	Leu		
				205					210		
Arg	Ile	Tyr	Arg	Asp	Asn	Lys	Thr	Ile	Asn		
				215					220		

Ser Glu Asn Met His Ile Asp Ile Tyr Leu
225 230

Tyr Thr Ser

(6) INFORMATION FOR SEQUENCE ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1712
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAAC TAGGTA	GAAAAATAAT	TATGAGAAAA	CACTATGTTG	40
TTAAAGATGT	TTTCGTATAT	AAGTTTAGGT	GATGTATAGT	80
TACTTAATTT	TAAAAGCATA	ACTTAATTAA	TATAAATAAC	120
ATGAGATTAT	TAAATATAAT	TAAGTTTCTT	TTAATGTTTT	160
TTTAATTGAA	TATTTAAGAT	TATAACATAT	ATTTAAAGTG	200
TATCTAGATA	CTTTTGGGA	ATGTTGGATA	AAGGAGATAA	240
AAAATGTATA	AGAGATTATT	TATTTACACAT	GTAATTTTGA	280
TATTCGCACT	GATATTAGTT	ATTTCTACAC	CCAACGTTTT	320
AGCAGAGAGT	CAACCAGATC	CTAAACCAGA	TGAGTTGCAC	360
AAATCGAGTA	AATTCACTGG	TTTGATGGAA	GATATGAAAG	400
TTTTGTATGA	TGATAATCAT	GTATCAGCAA	TAAACGTAA	440
ATCTATAGAT	CAATTCTAT	ACTTTGACTT	AATATATTCT	480
ATTAAGGACA	CTAAGTTAGG	GGATTATGAT	AATGTTCGAG	520
TCGAATTTAA	AAACAAAGAT	TTAGCTGATA	AATACAAAGA	560
TAAATACGTA	GATGTGTTTG	GAGCTAATTA	TTATTATCAA	600
TGTTATTTTT	CTAAAAAAC	GAATGATATT	AATTCGCATC	640
AAACTGACAA	ACGAAAAACT	TGTATGTATG	GTGGTGTAAC	680

TGAGCATAAT	GGAAACCAAT	TAGATAAATA	TAGAAGTATT	720
ACTGTTCTGGG	TATTTGAAGA	TGGTAAAAAT	TTATTATCTT	760
TTGACGTACA	AACTAATAAG	AAAAAGGTGA	CTGCTCAAGA	800
ATTAGATTAC	CTAACTCGTC	ACTATTTGGT	GAAAAATAAA	840
AAACTCTATG	AATTTAACAA	CTCGCCTTAT	GAAACGGGAT	880
ATATTAAATT	TATAGAAAAT	GAGAATAGCT	TTTGGTATGA	920
CATGATGCCT	GCACCAGGAG	ATAAATTTGC	CCAATCTAAA	960
TATTTAATGA	TGTACAATGA	CAATAAAATG	GTTGATTCTA	1000
AAGATGTGAA	GATTGAAGTT	TATCTTACGA	CAAAGAAAAA	1040
GTGAAATTAT	ATTTTAGAAA	AGTAAATATG	AAGAGTTAGT	1080
AATTAAGGCA	GGCACTTATA	GAGTACCTGC	CTTTTCTAAT	1120
ATTATTTAGT	TATAGTTATT	TTTGTTATAT	CTCTCTGATT	1160
TAGCATTAAC	CCCTTGTTGC	CATTATAGTT	TTCACCAACT	1200
TTAGCTGAAA	TTGGGGGATC	ATTTTTATCT	TTACTATGGA	1240
TAGTTACTGT	GTCGCCGTTT	TTAACGATTT	GTTTCTCTTT	1280
TAATTTGTCA	GTTAATTTTT	TCCATGCATC	ATTTGCGTCA	1320
AACCTATTTT	CATTTGGATT	TATTCTTGAC	AAATCAATTC	1360
TTTTAACACT	ATCGGTATTA	ATCGGCTTGT	TATTAAAATT	1400
ACTAAGTTCA	TCTAAATCAG	CTGTACCCGT	AATACTACTT	1440
TCGCCACCAT	TATTTAAATT	GTACGTAACA	CCAACTGTCT	1480
CATTTGCTGT	TTTATCGATA	ATATTTGCTT	CTTCAAAGC	1520
ATCTCTTACA	TTTTTCCATA	AGTCTCTATC	TGTTATTTCA	1560
GAAGCCTTTG	CAACGTTATT	AATACCATTA	TAATTTGAAG	1600
AAGAATGAAA	ACCTGAACCT	ACTGTTGTTA	AAACTAAAGC	1640
ACTTGCTATC	AATGTTCTTG	TTAATAGTTT	TTTATTCATT	1680
TTATTTTCTC	CTATAACTTA	TTTGCAATCG	AT	1712

(7) INFORMATION FOR SEQUENCE ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Tyr	Lys	Arg	Leu	Phe	Ile	Ser	His	Val		
				5					10		
Ile	Leu	Ile	Phe	Ala	Leu	Ile	Leu	Val	Ile		
				15					20		
Ser	Thr	Pro	Asn	Val	Leu	Ala	Glu	Ser	Gln		
				25					30		
Pro	Asp	Pro	Lys	Pro	Asp	Glu	Leu	His	Lys		
				35					40		
Ser	Ser	Lys	Phe	Thr	Gly	Leu	Met	Glu	Asp		
				45					50		
Met	Lys	Val	Leu	Tyr	Asp	Asp	Asn	His	Val		
				55					60		
Ser	Ala	Ile	Asn	Val	Lys	Ser	Ile	Asp	Gln		
				65					70		
Phe	Leu	Tyr	Phe	Asp	Leu	Ile	Tyr	Ser	Ile		
				75					80		
Lys	Asp	Thr	Lys	Leu	Gly	Asp	Tyr	Asp	Asn		
				85					90		
Val	Arg	Val	Glu	Phe	Lys	Asn	Lys	Asp	Leu		
				95					100		
Ala	Asp	Lys	Tyr	Lys	Asp	Lys	Tyr	Val	Asp		
				105					110		
Val	Phe	Gly	Ala	Asn	Tyr	Tyr	Tyr	Gln	Cys		
				115					120		
Tyr	Phe	Ser	Lys	Lys	Thr	Asn	Asp	Ile	Asn		
				125					130		
Ser	His	Gln	Thr	Asp	Lys	Arg	Lys	Thr	Cys		
				135					140		

Met	Tyr	Gly	Gly	Val	Thr	Glu	His	Asn	Gly		145	150
Asn	Gln	Leu	Asp	Lys	Tyr	Arg	Ser	Ile	Thr		155	160
Val	Arg	Val	Phe	Glu	Asp	Gly	Lys	Asn	Leu		165	170
Leu	Ser	Phe	Asp	Val	Gln	Thr	Asn	Lys	Lys		175	180
Lys	Val	Thr	Ala	Gln	Glu	Leu	Asp	Tyr	Leu		185	190
Thr	Arg	His	Tyr	Leu	Val	Lys	Asn	Lys	Lys		195	200
Leu	Tyr	Glu	Phe	Asn	Asn	Ser	Pro	Tyr	Glu		205	210
Thr	Gly	Tyr	Ile	Lys	Phe	Ile	Glu	Asn	Glu		215	220
Asn	Ser	Phe	Trp	Tyr	Asp	Met	Met	Pro	Ala		225	230
Pro	Gly	Asp	Lys	Phe	Ala	Gln	Ser	Lys	Tyr		235	240
Leu	Met	Met	Tyr	Asn	Asp	Asn	Lys	Met	Val		245	250
Asp	Ser	Lys	Asp	Val	Lys	Ile	Glu	Val	Tyr		255	260
Leu	Thr	Thr	Lys	Lys	Lys						265	

(8) INFORMATION FOR SEQUENCE ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1712
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAC TAGGTA GAAAAATAAT TATGAGAAAA CACTATGTTG

40

TTAAAGATGT TTTCGTATAT AAGTTTAGGT GATGTATAGT	80
TACTTAATTT TAAAAGCATA ACTTAATTAA TATAAATAAC	120
ATGAGATTAT TAAATATAAT TAAGTTTCTT TTAATGTTTT	160
TTTAATTGAA TATTTAAGAT TATAACATAT ATTTAAAGTG	200
TATCTAGATA CTTTTTGGGA ATGTTGGATA AAGGAGATAA	240
AAAATGTATA AGAGATTATT TATTTACAT GTAATTTTGA	280
TATTCGCACT GATATTAGTT ATTTCTACAC CCAACGTTTT	320
AGCAGAGAGT CAACCAGATC CTAAACCAGA TGAGTTGCAC	360
AAATCGAGTA AATTCACTGG TTTGATGGAA AATATGAAAG	400
TTTTGTATGA TGATAATCAT GTATCAGCAA TAAACGTAA	440
ATCTATAGAT CAATTTGAT ACTTTGACTT AATATATTCT	480
ATTAAGGACA CTAAGTTAGG GAATTATGAT AATGTTGAG	520
TCGAATTTAA AAACAAAGAT TTAGCTGATA AATACAAAGA	560
TAAATACGTA GATGTGTTTG GAGCTAATGC TTATTATCAA	600
TGTGCTTTTT CTAAAAAAC GAATGATATT AATTCGCATC	640
AAACTGACAA ACGAAAACT TGTATGTATG GTGGTGTAAC	680
TGAGCATAAT GGAAACCAAT TAGATAAATA TAGAAGTATT	720
ACTGTTCTGGG TATTTGAAGA TGGTAAAAAT TTATTATCTT	760
TTGACGTACA AACTAATAAG AAAAAGGTGA CTGCTCAAGA	800
ATTAGATTAC CTAACCTGTC ACTATTGGT GAAAAATAAA	840
AAACTCTATG AATTTAACA CTCGCCTTAT GAAACGGGAT	880
ATATTAAATT TATAGAAAAT GAGAATAGCT TTTGGTATGA	920
CATGATGCCCT GCACCAGGAG ATAAATTGA CCAATCTAAA	960
TATTTAATGA TGTACAATGA CAATAAAATG GTTGATTCTA	1000
AAGATGTGAA GATTGAAGTT TATCTTACGA CAAAGAAAAA	1040
GTGAAATTAT ATTTTAGAAA AGTAAATATG AAGAGTTAGT	1080
AATTAAGGCA GGCACCTATA GAGTACCTGC CTTTTCTAAT	1120

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ATTATTTAGT TATAGTTATT TTTGTTATAT CTCTCTGATT 1160
TAGCATTAAAC CCCTTGTTGC CATTATAGTT TTCACCAACT 1200
TTAGCTGAAA TTGGGGGATC ATTTTATCTT TTAATATGGA 1240
TAGTTACTGT GTCGCCGTTT TTAACGATTT GTTTCTCTTT 1280
TAATTTGTCA GTTAATTTTT TCCATGCATC ATTTGCGTCA 1320
AACCTATTTT CATTTGGATT TATTCTTGAC AAATCAATTC 1360
TTTTAACACT ATCGGTATTA ATCGGCTTGT TATTAAAATT 1400
ACTAAGTTCA TCTAAATCAG CTGTACCCGT AATACTACTT 1440
TCGCCACCAT TATTTAAATT GTACGTAACA CCAACTGTCT 1480
CATTTGCTGT TTTATCGATA ATATTGCTT CTTTCAAAGC 1520
ATCTCTTACA TTTTTCATA AGTCTCTATC TGTTATTTCA 1560
GAAGCCTTTG CAACGTTATT AATACCATTA TAATTTGAAG 1600
AAGAATGAAA ACCTGAACCT ACTGTTGTTA AACTAAAGC 1640
ACTTGCTATC AATGTTCTTG TTAATAGTTT TTTATTCATT 1680
TTATTTTCTC CTATAACTTA TTTGCAATCG AT 1712

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(9) INFORMATION FOR SEQUENCE ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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Met Tyr Lys Arg Leu Phe Ile Ser His Val
                    5                      10

Ile Leu Ile Phe Ala Leu Ile Leu Val Ile
                    15                      20

Ser Thr Pro Asn Val Leu Ala Glu Ser Gln
                    25                      30

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Pro	Asp	Pro	Lys	Pro	Asp	Glu	Leu	His	Lys	
				35					40	
Ser	Ser	Lys	Phe	Thr	Gly	Leu	Met	Glu	Asn	
				45					50	
Met	Lys	Val	Leu	Tyr	Asp	Asp	Asn	His	Val	
				55					60	
Ser	Ala	Ile	Asn	Val	Lys	Ser	Ile	Asp	Gln	
				65					70	
Phe	Arg	Tyr	Phe	Asp	Leu	Ile	Tyr	Ser	Ile	
				75					80	
Lys	Asp	Thr	Lys	Leu	Gly	Asn	Tyr	Asp	Asn	
				85					90	
Val	Arg	Val	Glu	Phe	Lys	Asn	Lys	Asp	Leu	
				95					100	
Ala	Asp	Lys	Tyr	Lys	Asp	Lys	Tyr	Val	Asp	
				105					110	
Val	Phe	Gly	Ala	Asn	Ala	Tyr	Tyr	Gln	Cys	
				115					120	
Ala	Phe	Ser	Lys	Lys	Thr	Asn	Asp	Ile	Asn	
				125					130	
Ser	His	Gln	Thr	Asp	Lys	Arg	Lys	Thr	Cys	
				135					140	
Met	Tyr	Gly	Gly	Val	Thr	Glu	His	Asn	Gly	
				145					150	
Asn	Gln	Leu	Asp	Lys	Tyr	Arg	Ser	Ile	Thr	
				155					160	
Val	Arg	Val	Phe	Glu	Asp	Gly	Lys	Asn	Leu	
				165					170	
Leu	Ser	Phe	Asp	Val	Gln	Tyr	Asn	Lys	Lys	
				175					180	
Lys	Val	Thr	Ala	Gln	Glu	Leu	Asp	Tyr	Leu	
				185					190	
Thr	Arg	His	Tyr	Leu	Val	Lys	Asn	Lys	Lys	
				195					200	
Leu	Tyr	Glu	Phe	Asn	Asn	Ser	Pro	Tyr	Glu	
				205					210	

Thr	Gly	Tyr	Ile	Lys	Phe	Ile	Glu	Asn	Glu		
				215					220		
Asn	Ser	Phe	Trp	Tyr	Asp	Met	Met	Pro	Ala		
				225					230		
Pro	Gly	Asp	Lys	Phe	Asp	Gln	Ser	Lys	Tyr		
				235					240		
Leu	Met	Met	Tyr	Asn	Asp	Asn	Lys	Met	Val		
				245					250		
Asp	Ser	Lys	Asp	Val	Lys	Ile	Glu	Val	Tyr		
				255					260		
Leu	Thr	Thr	Lys	Lys	Lys						
				265							

(10) INFORMATION FOR SEQUENCE ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1388
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAGTCAAC CAGATCCTAA ACCAGATGAG TTGCACAAAT	40
CGAGTAAATT CACTGGTTTG ATGGAAAATA TGAAAGTTTT	80
GTATGATGAT AATCATGTAT CAGCAATAAA CGTTAAATCT	120
ATAGATCAAT TTCGATACTT TGACTTAATA TATTCTATTA	160
AGGACACTAA GTTAGGGAAT TATGATAATG TTCGAGTCGA	200
ATTTAAAAAC AAAGATTTAG CTGATAAATA CAAAGATAAA	240
TACGTAGATG TGTTTGGAGC TAATGCTTAT TATCAATGTG	280
CTTTTTCTAA AAAAACGAAT GATATTAATT CGCATCAAAC	320
TGACAAACGA AAAACTTGTA TGTATGGTGG TGTAAGTGAG	360
CATAATGGAA ACCAATTAGA TAAATATAGA AGTATTACTG	400
TTCGGGTATT TGAAGATGGT AAAAATTTAT TATCTTTTGA	440

CGTACAAACT AATAAGAAAA AGGTGACTGC TCAAGAATTA	480
GATTACCTAA CTCGTCAC TA TTTGGTGAAA AATAAAAAAC	520
TCTATGAATT TAACAAC TCG CCTTATGAAA CGGGATATAT	560
TAAATTTATA GAAAATGAGA ATAGCTTTTG GTATGACATG	600
ATGCCTGCAC CAGGAGATAA ATTTGACCAA TCTAAATATT	640
TAATGATGTA CAATGACAAT AAAATGGTTG ATTCTAAAGA	680
TGTGAAGATT GAAGTTTATC TTACGACAAA GAAAAAGTGA	720
AATTATATTT TAGAAAAGTA AATATGAAGA GTTAGTAATT	760
AAGGCAGGCA CTTATAGAGT ACCTGCCTTT TCTAATATTA	800
TTTAGTTATA GTTATTTTTG TTATATCTCT CTGATTTAGC	840
ATTAACCCCT TGTTGCCATT ATAGTTTTTCAC CAACTTTAG	880
CTGAAATTGG GGGATCATTT TTATCTTTAC TATGGATAGT	920
TACTGTGTCG CCGTTTTTAA CGATTTGTTT CTCTTTTAAT	960
TTGTCAGTTA ATTTTTTCCA TGCATCATTT GCGTCAAACC	1000
TATTTCCATT TGGATTTATT CTTGACAAAT CAATTCTTTT	1040
AACACTATCG GTATTAATCG GCTTGTTATT AAAATTACTA	1080
AGTTCATCTA AATCAGCTGT ACCCGTAATA CTACTTTCGC	1120
CACCATTATT TAAATTGTAC GTAACACCAA CTGTCTCATT	1160
TGCTGTTTTA TCGATAATAT TTGCTTCTTT CAAAGCATCT	1200
CTTACATTTT TCCATAAGTC TCTATCTGTT ATTTCAGAAG	1240
CCTTTGCAAC GTTATTAATA CCATTATAAT TTGAAGAAGA	1280
ATGAAAACCT GAACCTACTG TTGTTAAAAC TAAAGCACTT	1320
GCTATCAATG TTCTTGTTAA TAGTTTTTTT TTCATTTTAT	1360
TTTCTCCTAT AACTTATTTG CAATCGAT	1388

(11) INFORMATION FOR SEQUENCE ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239

(B) TYPE: Amino Acid
 (C) STRANDEDNESS: Unknown
 (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ser	Gln	Pro	Asp	Pro	Lys	Pro	Asp	Glu	5	10
Leu	His	Lys	Ser	Ser	Lys	Phe	Thr	Gly	Leu	15	20
Met	Glu	Asn	Met	Lys	Val	Leu	Tyr	Asp	Asp	25	30
Asn	His	Val	Ser	Ala	Ile	Asn	Val	Lys	Ser	35	40
Ile	Asp	Gln	Phe	Arg	Tyr	Phe	Asp	Leu	Ile	45	50
Tyr	Ser	Ile	Lys	Asp	Thr	Lys	Leu	Gly	Asn	55	60
Tyr	Asp	Asn	Val	Arg	Val	Glu	Phe	Lys	Asn	65	70
Lys	Asp	Leu	Ala	Asp	Lys	Tyr	Lys	Asp	Lys	75	80
Tyr	Val	Asp	Val	Phe	Gly	Ala	Asn	Ala	Tyr	85	90
Tyr	Gln	Cys	Ala	Phe	Ser	Lys	Lys	Thr	Asn	95	100
Asp	Ile	Asn	Ser	His	Gln	Thr	Asp	Lys	Arg	105	110
Lys	Thr	Cys	Met	Tyr	Gly	Gly	Val	Thr	Glu	115	120
His	Asn	Gly	Asn	Gln	Leu	Asp	Lys	Tyr	Arg	125	130
Ser	Ile	Thr	Val	Arg	Val	Phe	Glu	Asp	Gly	135	140
Lys	Asn	Leu	Leu	Ser	Phe	Asp	Val	Gln	Thr	145	150
Asn	Lys	Lys	Lys	Val	Thr	Ala	Gln	Glu	Leu		

	155		160
Asp Tyr Leu Thr Arg His Tyr Leu Val Lys			
	165		170
Asn Lys Lys Leu Tyr Glu Phe Asn Asn Ser			
	175		180
Pro Tyr Glu Thr Gly Tyr Ile Lys Phe Ile			
	185		190
Glu Asn Glu Asn Ser Phe Trp Tyr Asp Met			
	195		200
Met Pro Ala Pro Gly Asp Lys Phe Asp Gln			
	205		210
Ser Lys Tyr Leu Met Met Tyr Asn Asp Asn			
	215		220
Lys Met Val Asp Ser Lys Asp Val Lys Ile			
	225		230
Glu Val Tyr Leu Thr Thr Lys Lys Lys			
	235		

(12) INFORMATION FOR SEQUENCE ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAAGGAGAAT TAAAAATGAA TAAAAAATTA CTAATGAATT	40
TTTTTATCGT AAGCCCTTTG TTGCTTGCGA CAACTGCTAC	80
AGATTTTACC CCTGTTCCCT TATCATCTAA TCAAATAATC	120
AAAACTGCAA AAGCATCTAC AAACGATAAT ATAAAGGATT	160
TGCTAGACTG GTATAGTAGT GGGTCTGACA CTTTTACAAA	200
TAGTGAAGTT TTAGATAATT CCAGAGGATC TATGCGTATA	240
AAAAACACAG ATGGCAGCAT CAGCTTGATA ATTTTCCGA	280

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GTCCTTATTA TAGCCCTGCT TTTACAAAAG GGGAAAAAGT    320
TGACTTAAAC ACAAAAAGAA CTAAAAAAG CCAACATACT    360
AGCGAAGGAA CTTATATCCA TTTCCAAATA AGTGGCGTTA    400
CAAATACTGA AAAATTACCT ACTCCAATAG AACTACCTTT    440
AAAAGTTAAG GTTCATGGTA AAGATAGCCC CTTAAAGTAT    480
GGGCCAAAGT TCGATAAAAA ACAATTAGCT ATATCAACTT    520
TAGACTTTGA AATTCGTCAT CAGCTAACTC AAATACATGG    560
ATTATATCGT TCAAGCGATA AAACGGGTGG TTATTGGAAA    600
ATAACAATGA ATGACGGATC CACATATCAA AGTGATTTAT    640
CTAAAAAGTT TGAATACAAT ACTGAAAAAC CACCTATAAA    680
TATTGATGAA ATAAAAACTA TAGAAGCAGA AATTAATTAA    720
TTTACCACTT T                                     731

```

(13) INFORMATION FOR SEQUENCE ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Met Asn Lys Lys Leu Leu Met Asn Phe Phe
      5                                10

```

```

Ile Val Ser Pro Leu Leu Leu Ala Thr Thr
      15                            20

```

```

Ala Thr Asp Phe Thr Pro Val Pro Leu Ser
      25                            30

```

```

Ser Asn Gln Ile Ile Lys Thr Ala Lys Ala
      35                            40

```

```

Ser Thr Asn Asp Asn Ile Lys Asp Leu Leu
      45                            50

```

```

Asp Trp Tyr Ser Ser Gly Ser Asp Thr Phe
      55                            60

```

Thr	Asn	Ser	Glu	Val 65	Leu	Asp	Asn	Ser	Arg 70
Gly	Ser	Met	Arg	Ile 75	Lys	Asn	Thr	Asp	Gly 80
Ser	Ile	Ser	Leu	Ile 85	Ile	Phe	Pro	Ser	Pro 90
Tyr	Tyr	Ser	Pro	Ala 95	Phe	Thr	Lys	Gly	Glu 100
Lys	Val	Asp	Leu	Asn 105	Thr	Lys	Arg	Thr	Lys 110
Lys	Ser	Gln	His	Thr 115	Ser	Glu	Gly	Thr	Tyr 120
Ile	His	Phe	Gln	Ile 125	Ser	Gly	Val	Thr	Asn 130
Thr	Glu	Lys	Leu	Pro 135	Thr	Pro	Ile	Glu	Leu 140
Pro	Leu	Lys	Val	Lys 145	Val	His	Gly	Lys	Asp 150
Ser	Pro	Leu	Lys	Tyr 155	Gly	Pro	Lys	Phe	Asp 160
Lys	Lys	Gln	Leu	Ala 165	Ile	Ser	Thr	Leu	Asp 170
Phe	Glu	Ile	Arg	His 175	Gln	Leu	Thr	Gln	Ile 180
His	Gly	Leu	Tyr	Arg 185	Ser	Ser	Asp	Lys	Thr 190
Gly	Gly	Tyr	Trp	Lys 195	Ile	Thr	Met	Asn	Asp 200
Gly	Ser	Thr	Tyr	Gln 205	Ser	Asp	Leu	Ser	Lys 210
Lys	Phe	Glu	Tyr	Asn 215	Thr	Glu	Lys	Pro	Pro 220
Ile	Asn	Ile	Asp	Glu 225	Ile	Lys	Thr	Ile	Glu 230
Ala	Glu	Ile	Asn						

(14) INFORMATION FOR SEQUENCE ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATCATTAAT ATAATTAATT TTCTTTTAAT ATTTTTTTAA	40
TTGAATATTT AAGATTATAA GATATATTTA AAGTGATCT	80
AGATACTTTT TGGGAATGTT GGATGAAGGA GATAAAAATG	120
AATAAGAGTC GATTTATTTT ATGCGTAATT TTGATATTCG	160
CACTTATACT AGTTCTTTTT ACACCCAACG TATTAGCAGA	200
GAGCCAACCA GACCCTACGC CAGATGAGTT GCACAAAGCG	240
AGTAAATTCA CTGGTTTGAT GGAAAATATG AAAGTTTAT	280
ATGATGATCA TTATGTATCA GCAACTAAAG TTAAGTCTGT	320
AGATAAATTT AGGGCACATG ATTTAATTTA TAACATTAGT	360
GATAAAAAAC TGAAAAATTA TGACAAAGTG AAAACAGAGT	400
TATTAAATGA AGGTTTAGCA AAGAAGTACA AAGATGAAGT	440
AGTTGATGTG TATGGATCAA ATTACTATGT AACTGCTAT	480
TTTTCATCCA AAGATAATGT AGGTAAAGTT ACAGGTGGCA	520
AACTTGTAT GTATGGAGGA ATAACAAAAC ATGAAGGAAA	560
CCACTTTGAT AATGGGAACT TACAAAATGT ACTTATAAGA	600
GTTTATGAAA ATAAAAGAAA CACAATTTCT TTTGAAGTGC	640
AACTGATAA GAAAAGTGTA ACAGCTCAAG AACTAGACAT	680
AAAAGCTAGG AATTTTTTTAA TTAATAAAAA AAATTTGTAT	720
GAGTTTAACA GTTCACCATA TGAAACAGGA TATATAAAAT	760
TTATTGAAAA TAACGGCAAT ACTTTTTTGGT ATGATATGAT	800

```

GCCTGCACCA GGCATAAGT TTGACCAATC TAAATATTTA      840
ATGATGTACA ACGACAATAA AACGGTTGAT TCTAAAAGTG      880
TGAAGATAGA AGTCCACCTT ACAACAAAGA ATGGATAATG      920
TTAATCCGAT TTTGATATAA AAAGTGAAAG TATTAGATAT      960
ATTTGAAAGG TAAGTACTTC GGTGCTTGCC TTTT TAGGAT     1000
GCATATATAT AGATTAAACC GCACTTCTAT ATTAATAGAA     1040
AGTGCGGTTA TTTATACACT CAATCTAAAC TATAATAATT     1080
GGAATCATCT TCAAA                                  1095

```

(15) INFORMATION FOR SEQUENCE ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Met Asn Lys Ser Arg Phe Ile Ser Cys Val
      5                                10
Ile Leu Ile Phe Ala Leu Ile Leu Val Leu
      15                             20
Phe Thr Pro Asn Val Leu Ala Glu Ser Gln
      25                             30
Pro Asp Pro Thr Pro Asp Glu Leu His Lys
      35                             40
Ala Ser Lys Phe Thr Gly Leu Met Glu Asn
      45                             50
Met Lys Val Leu Tyr Asp Asp His Tyr Val
      55                             60
Ser Ala Thr Lys Val Lys Ser Val Asp Lys
      65                             70
Phe Arg Ala His Asp Leu Ile Tyr Asn Ile
      75                             80

```

Ser	Asp	Lys	Lys	Leu	Lys	Asn	Tyr	Asp	Lys	
				85					90	
Val	Lys	Thr	Glu	Leu	Leu	Asn	Glu	Gly	Leu	
				95					100	
Ala	Lys	Lys	Tyr	Lys	Asp	Glu	Val	Val	Asp	
				105					110	
Val	Tyr	Gly	Ser	Asn	Tyr	Tyr	Val	Asn	Cys	
				115					120	
Tyr	Phe	Ser	Ser	Lys	Asp	Asn	Val	Gly	Lys	
				125					130	
Val	Thr	Gly	Gly	Lys	Thr	Cys	Met	Tyr	Gly	
				135					140	
Gly	Ile	Thr	Lys	His	Glu	Gly	Asn	His	Phe	
				145					150	
Asp	Asn	Gly	Asn	Leu	Gln	Asn	Val	Leu	Ile	
				155					160	
Arg	Val	Tyr	Glu	Asn	Lys	Arg	Asn	Thr	Ile	
				165					170	
Ser	Phe	Glu	Val	Gln	Thr	Asp	Lys	Lys	Ser	
				175					180	
Val	Thr	Ala	Gln	Glu	Leu	Asp	Ile	Lys	Ala	
				185					190	
Arg	Asn	Phe	Leu	Ile	Asn	Lys	Lys	Asn	Leu	
				195					200	
Tyr	Glu	Phe	Asn	Ser	Ser	Phe	Tyr	Glu	Thr	
				205					210	
Gly	Tyr	Ile	Lys	Phe	Ile	Glu	Asn	Asn	Gly	
				215					220	
Asn	Thr	Phe	Trp	Tyr	Asp	Met	Met	Pro	Ala	
				225					230	
Pro	Gly	Asp	Lys	Phe	Asp	Gln	Ser	Lys	Tyr	
				235					240	
Leu	Met	Met	Tyr	Asn	Asp	Asn	Lys	Thr	Val	
				245					250	
Asp	Ser	Lys	Ser	Val	Lys	Ile	Glu	Val	His	
				255					260	

Leu Thr Thr Lys Asn Gly
265

(16) INFORMATION FOR SEQUENCE ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1837
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCATGTTTGA CAGCTTATCA TCGATAAGCT TACTTTTCGA	40
ATCAGGTCTA TCCTTGAAAC AGGTGCAACA TAGATTAGGG	80
CATGGAGATT TACCAGACAA CTATGAACGT ATATACTCAC	120
ATCACGCAAT CGGCAATTGA TGACATTGGA ACTAAATTCA	160
ATCAATTTGT TACTAACAAG CAACTAGATT GACAACATAAT	200
TCTCAACAAA CGTTAATTTA ACAACATTCA AGTAACTCCC	240
ACCAGCTCCA TCAATGCTTA CCGTAAGTAA TCATAACTTA	280
CTAAACCTT GTTACATCAA GGTTTTTTCT TTTTGTCTTG	320
TTCATGAGTT ACCATAACTT TCTATATTAT TGACAACTAA	360
ATTGACAACT CTTCAATTAT TTTTCTGTCT ACTCAAAGTT	400
TTCTTCATTT GATATAGTCT AATTCCACCA TCACTTCTTC	440
CACTCTCTCT ACCGTCACAA CTTTCATCATC TCTCACTTTT	480
TCGTGTGGTA ACACATAATC AAATATCTTT CCGTTTTTAC	520
GCACTATCGC TACTGTGTCA CCTAAAATAT ACCCCTTATC	560
AATCGCTTCT TTAAACTCAT CTATATATAA CATATTTTCA	600
CCTCCTACCT ATCTATTCGT AAAAAGATAA AAATAACTAT	640
TGTTTTTTTT GTTATTTTAT AATAAAATTA TTAATATAAG	680
TTAATGTTTT TTAAAAATAT ACAATTTTAT TCTATTTATA	720

GTTAGCTATT	TTTTCATTGT	TAGTAATATT	GGTGAATTGT	760
AATAACCTTT	TTAAATCTAG	AGGAGAACCC	AGATATAAAA	800
TGGAGGAATA	TTAATGGAAA	ACAATAAAAA	AGTATTGAAG	840
AAAATGGTAT	TTTTTGTTTT	AGTGACATTT	CTTGACTAA	880
CAATCTCGCA	AGAGGTATTT	GCTCAACAAG	ACCCCGATCC	920
AAGCCAACTT	CACAGATCTA	GTTTAGTTAA	AAACCTTCAA	960
AATATATATT	TTCTTTATGA	GGTGACCCT	GTTACTCACG	1000
AGAATGTGAA	ATCTGTTGAT	CAACTTAGAT	CTCACGATTT	1040
AATATATAAT	GTTTCAGGGC	CAAATTATGA	TAAATTAAAA	1080
ACTGAACTTA	AGAACCAAGA	GATGGCAACT	TTATTTAAGG	1120
ATAAAAACGT	TGATATTTAT	GGTGTAGAAT	ATTACCATCT	1160
CTGTTATTTA	TGTGAAAATG	CAGAAAGGAG	TGCATGTATC	1200
TACGGAGGGG	TAACAAATCA	TGAAGGGAAT	CATTTAGAAA	1240
TTCCATAAAA	GATAGTCGTT	AAAGTATCAA	TCGATGGTAT	1280
CCAAAGCCTA	TCATTTGATA	TTGAAACAAA	TAAAAAATG	1320
GTAAC TGCTC	AAGAATTAGA	CTATAAAGTT	AGAAAATATC	1360
TTACAGATAA	TAAGCAACTA	TATACTAATG	GACCTTCTAA	1400
ATATGAACT	GGATATATAA	AGTTCATACC	TAAGAATAAA	1440
GAAAGTTTTT	GGTTTGATTT	TTTCCCTGAA	CCAGAATTTA	1480
CTCAATCTAA	ATATCTTATG	ATATATAAAG	ATAATGAAAC	1520
GCTTGACTCA	AACACAAGCC	AAATTGAAGT	CTACCTAACA	1560
ACCAAGTAAC	TTTTTGCTTT	TGGCAACCTT	ACCTACTGCT	1600
GGATTTAGAA	ATTTTATTGC	AATTCTTTTA	TTAATGTAAA	1640
AACCGCTCAT	TTGATGAGCG	GTTTTGTCTT	ATCTAAAGGA	1680
GCTTTACCTC	CTAATGCTGC	AAAATTTTAA	ATGTTGGATT	1720
TTTGTATTTG	TCTATTGTAT	TTGATGGGTA	ATCCCATTTT	1760
TCGACAGACA	TCGTCGTGCC	ACCTCTAACA	CCAAAATCAT	1800

AGACAGGAGC TTGTAGCTTA GCAACTATTT TATCGTC

1837

(17) INFORMATION FOR SEQUENCE ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Glu Asn Asn Lys Lys Val Leu Lys Lys
5 10

Met Val Phe Phe Val Leu Val Thr Phe Leu
15 20

Gly Leu Thr Ile Ser Gln Glu Val Phe Ala
25 30

Gln Gln Asp Pro Asp Pro Ser Gln Leu His
35 40

Arg Ser Ser Leu Val Lys Asn Leu Gln Asn
45 50

Ile Tyr Phe Leu Tyr Glu Gly Asp Pro Val
55 60

Thr His Glu Asn Val Lys Ser Val Asp Gln
65 70

Leu Arg Ser His Asp Leu Ile Tyr Asn Val
75 80

Ser Gly Pro Asn Tyr Asp Lys Leu Lys Thr
85 90

Glu Leu Lys Asn Gln Glu Met Ala Thr Leu
95 100

Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly
105 110

Val Glu Tyr Tyr His Leu Cys Tyr Leu Cys
115 120

Glu Asn Ala Glu Arg Ser Ala Cys Ile Tyr
125 130

Gly Gly Val Thr Asn His Glu Gly Asn His

	135		140
Leu Glu Ile Pro	Lys Lys Ile Val Val	Lys	
	145		150
Val Ser Ile Asp	Gly Ile Gln Ser Leu	Ser	
	155		160
Phe Asp Ile Glu	Thr Asn Lys Lys Met	Val	
	165		170
Thr Ala Gln Glu	Leu Asp Tyr Lys Val	Arg	
	175		180
Lys Tyr Leu Thr	Asp Asn Lys Gln Leu	Tyr	
	185		190
Thr Asn Gly Pro	Ser Lys Tyr Glu Thr	Gly	
	195		200
Tyr Ile Lys Phe	Ile Pro Lys Asn Lys	Glu	
	205		210
Ser Phe Trp Phe	Asp Phe Phe Pro Glu	Pro	
	215		220
Glu Phe Thr Gln	Ser Lys Tyr Leu Met	Ile	
	225		230
Tyr Lys Asp Asn	Glu Thr Leu Asp Ser	Asn	
	235		240
Thr Ser Gln Ile	Glu Val Tyr Leu Thr	Thr	
	245		250

Lys

(18) INFORMATION FOR SEQUENCE ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82

(B) TYPE: Amino Acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser His Asp Gln Phe Leu Gln His Thr Ile	
	5 10
Leu Phe Lys Gly Phe Phe Thr Asp His Ser	
	15 20
Trp Tyr Asn Asp Leu Leu Val Asp Phe Asp	
	25 30
Ser Lys Asp Ile Val Asp Lys Tyr Lys Gly	
	35 40

Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr
 45 50
 Gly Tyr Gln Cys Ala Gly Gly Thr Pro Asn
 55 60
 Lys Thr Ala Cys Met Tyr Gly Gly Val Thr
 65 70
 Leu His Asp Asn Asn Arg Leu Thr Glu Glu
 75 80
 Lys Lys

(19) INFORMATION FOR SEQUENCE ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Thr Gly Asp Gln Phe Leu Glu Asn Thr Leu
 5 10
 Leu Tyr Lys Lys Phe Phe Thr Asp Leu Ile
 15 20
 Asn Phe Glu Asp Leu Leu Ile Asn Phe Asn
 25 30
 Ser Lys Glu Met Ala Gln His Phe Lys Ser
 35 40
 Lys Asn Val Asp Val Tyr Pro Ile Arg Tyr
 45 50
 Ser Ile Asn Cys Tyr Gly Gly Glu Ile Asp
 55 60
 Arg Thr Ala Cys Thr Tyr Gly Gly Val Thr
 65 70
 Pro His Glu Gly Asn Lys Leu Lys Glu Arg
 75 80
 Lys Lys

(20) INFORMATION FOR SEQUENCE ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser Asp Asp Gln Phe Leu Glu Asn Thr Leu
 5 10
 Leu Phe Lys Gly Phe Phe Thr Gly His Pro
 15 20
 Trp Tyr Asn Asp Leu Leu Val Asp Leu Gly
 25 30
 Ser Lys Asp Ala Thr Asn Lys Tyr Lys Gly
 35 40
 Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr
 45 50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89
(B) TYPE: Amino Acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

(ii) Molecule type: Repetition										
Ser	Ile	Asp	Gln	Phe	Leu	Tyr	Phe	Asp	Leu	
				5						10
Ile	Tyr	Ser	Ile	Lys	Asp	Thr	Lys	Leu	Gly	
				15						20
Asn	Tyr	Asp	Asn	Val	Arg	Val	Glu	Phe	Lys	
				25						30
Asn	Lys	Asp	Leu	Ala	Asp	Lys	Tyr	Lys	Asp	
				35						40
Lys	Tyr	Val	Asp	Val	Phe	Gly	Ala	Asn	Tyr	
				45						50
Tyr	Gln	Cys	Tyr	Phe	Ser	Lys	Lys	Thr	Asn	
				55						60
Asp	Ile	Asn	Ser	His	Gln	Thr	Asp	Lys	Arg	
				65						70
Lys	Thr	Cys	Met	Tyr	Gly	Gly	Val	Thr	Glu	
				75						80
His	Asn	Gly	Asn	Gln	Leu	Asp	Lys	Tyr		
				85						

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89
(B) TYPE: Amino Acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser	Val	Asp	Lys	Phe	Leu	Ala	His	Asp	Leu	5	10
Ile	Tyr	Asn	Ile	Ser	Asp	Lys	Lys	Leu	Lys	15	20
Asn	Tyr	Asp	Lys	Val	Lys	Thr	Glu	Leu	Leu	25	30
Asn	Glu	Gly	Leu	Ala	Lys	Lys	Tyr	Lys	Asp	35	40
Glu	Val	Val	Asp	Val	Tyr	Gly	Ser	Asn	Tyr	45	50
Tyr	Val	Asn	Cys	Tyr	Phe	Ser	Ser	Lys	Asp		

	55	60
Asn Val Gly Lys	Val Thr Gly Gly Lys Thr	
	65	70
Cys Met Tyr Gly	Gly Ile Thr Lys His Glu	
	75	80
Gly Asn His Phe	Asp Asn Gly Asn Leu	
	85	

(23) INFORMATION FOR SEQUENCE ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser Val Asp Lys	Phe Leu Ala His Asp Leu	
	5	10
Ile Tyr Asn Ile	Ser Asp Lys Lys Leu Lys	
	15	20
Asn Tyr Asp Lys	Val Lys Thr Glu Leu Leu	
	25	30
Asn Glu Asp Leu	Ala Lys Lys Tyr Lys Asp	
	35	40
Glu Val Val Asp	Val Tyr Gly Ser Asn Tyr	
	45	50
Tyr Val Asn Cys	Tyr Phe Ser Ser Lys Asp	
	55	60
Asn Val Gly Lys	Val Thr Gly Gly Lys Thr	
	65	70
Cys Met Tyr Gly	Gly Ile Thr Lys His Glu	
	75	80
Gly Asn His Phe	Asp Asn Gly Asn Leu	
	85	

(24) INFORMATION FOR SEQUENCE ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser Val Asp Lys	Phe Leu Ala His Asp Leu	
	5	10
Ile Tyr Asn Ile	Ser Asp Lys Lys Leu Lys	
	15	20
Asn Tyr Asp Lys	Val Lys Thr Glu Leu Leu	
	25	30
Asn Glu Asp Leu	Ala Lys Lys Tyr Lys Asp	
	35	40
Glu Val Val Asp	Val Tyr Gly Ser Asn Tyr	
	45	50
Tyr Val Asn Cys	Tyr Phe Ser Ser Lys Asp	
	55	60

Asn Val Gly Lys Val Thr Gly Gly Lys Thr
 65 70
 Cys Met Tyr Gly Gly Ile Thr Lys His Glu
 75 80
 Gly Asn His Phe Asp Asn Gly Asn Leu
 85

(25) INFORMATION FOR SEQUENCE ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Ser Val Asp Gln Leu Leu Ser His Asp Leu
 5 10
 Ile Tyr Asn Val Ser Gly Pro Asn Tyr Asp
 15 20
 Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu
 25 30
 Met Ala Thr Leu Phe Lys Asp Lys Asn Val
 35 40
 Asp Ile Tyr Gly Val Glu Tyr Tyr His Leu
 45 50
 Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser
 55 60
 Ala Cys Ile Tyr Gly Gly Val Thr Asn His
 65 70
 Glu Gly Asn His Leu Glu Ile Pro Lys
 75

(26) INFORMATION FOR SEQUENCE ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) Molecule type: Peptide

Val Leu Asp Asn Ser Leu Gly Ser Met Arg
 5 10
 Ile Lys Asn Thr Asp Gly Ser Ile Ser Leu
 15 20
 Ile Ile Phe Pro Ser Pro Tyr Tyr Ser Pro
 25 30
 Ala Phe Thr Lys Gly Glu Lys Val Asp Leu
 35 40
 Asn Thr Lys Arg Thr Lys Lys Ser Gln His
 45 50
 Thr Ser Glu Gly Thr Tyr Ile His Phe Gln
 55 60
 Ile Ser Gly Val Thr Asn Thr Glu Lys Leu
 65 70
 Pro Thr Pro